

↓: is the regions for β -sheet deletions

*: is the N-linked glycosylation sites for subtype C TV1 and TV2. Possible mutation (N \rightarrow Q) or deletions can be performed.

		1		50
SF162	(1)	----MDAMKRG LCCVLLCCGAVFVSPSAVEK LNVTVVYGVFWRE K TTL		
TV1.8_2	(1)	MRVMGTQKNCQQWWIWGILGFWMLMICNTED LNVTVVYGVFWRE K TTL		
TV1.8_5	(1)	MRVMGTQKNCQQWWIWGILGFWMLMICNTED LNVTVVYGVFWRE K TTL		
TV2.12-5/1	(1)	MRARGILKNYRHHWWIWGILGFWMLMMC NVKGLNVTVVYGVFWRE K TTL		
Consensus	(1)	MRVMGTQKNCQQWWIWGILGFWMLMICNVED LNVTVVYGVFWRE K TTL		
		51	*	100
SF162	(47)	FCASDAKAYDTEVHNWATHACVPTDPNPQEIVLG NVTFNFMWKNMVD		
TV1.8_2	(51)	FCASDAKAYETEVHNWATHACVPTDPNPQEIVLG NVTFNFMWKNMVD		
TV1.8_5	(51)	FCASDAKAYETEVHNWATHACVPTDPNPQEIVLG NVTFNFMWKNMVD		
TV2.12-5/1	(51)	FCASDAKAYEKEVENWATHACVPTDPNPQEIVLG NVTFNFMWKNMVD		
Consensus	(51)	FCASDAKAYETEVHNWATHACVPTDPNPQEIVLG NVTFNFMWKNMVD		
		101	β 2/V1V2/ β 3	*
			↓	
SF162	(97)	QM HEDIISLWDQSLKPCVKLTPLCVTLNCTNTNVTGNRTVTGNSTNTNG		
TV1.8_2	(101)	QM HEDIISLWDQSLKPCVKLTPLCVTLNCTNTNVTGNRTVTGNSTNTNG		
TV1.8_5	(101)	QM HEDIISLWDQSLKPCVKLTPLCVTLNCTNTNVTGNRTVTGNSTNTNG		
TV2.12-5/1	(101)	QM QEDIISLWDQSLKPCVKLTPLCVTLNCTNTNVTGNRTVTGNSTNTNG		
Consensus	(101)	QM HEDIISLWDQSLKPCVKLTPLCVTLNCTNTNVTGNRTVTGNSTNTNG		
		151	*	*200
SF162	(139)	WKEMDRGEENKCSFYVTELDKKEENALFYKLDIVPLNN ENSNFTY		
TV1.8_2	(151)	TGIYNIEEMKNCSEYVTELDKKEENALFYKLDIVPLNN ENSNFTY		
TV1.8_5	(151)	NATYKYEEMKNCSEYVTELDKKEENALFYKLDIVPLNN ENSNFTY		
TV2.12-5/1	(141)	-----KEMKNCSEYVTELDKKEENALFYKLDIVPLNN ENSNFTY		
Consensus	(151)	A Y EEMKNCSEYVTELDKKEENALFYKLDIVPLNN ENSNFTY		
		201	*	*
			↓	
SF162	(185)	RLINCNSTSTITQACPKVSFDPIPIHYCAPAGYAILKCNKTFNGTGPCYN		
TV1.8_2	(199)	RLINCNSTSTITQACPKVSFDPIPIHYCAPAGYAILKCNKTFNGTGPCYN		
TV1.8_5	(199)	RLINCNSTSTITQACPKVSFDPIPIHYCAPAGYAILKCNKTFNGTGPCYN		
TV2.12-5/1	(185)	RLINCNSTSTITQACPKVSFDPIPIHYCAPAGYAILKCNKTFNGTGPCYN		
Consensus	(201)	RLINCNSTSTITQACPKVSFDPIPIHYCAPAGYAILKCNKTFNGTGPCYN		
		251	*	*
			↓	
SF162	(235)	VSTVQCTHGIRFVVSTQLLNGSLAEGIIIRSENLTENTKTIIIVHLNES		
TV1.8_2	(249)	VSTVQCTHGIRFVVSTQLLNGSLAEGIIIRSENLTENTKTIIIVHLNES		
TV1.8_5	(249)	VSTVQCTHGIRFVVSTQLLNGSLAEGIIIRSENLTENTKTIIIVHLNES		
TV2.12-5/1	(235)	VSTVQCTHGIRFVVSTQLLNGSLAEGIIIRSENLTENTKTIIIVHLNES		
Consensus	(251)	VSTVQCTHGIRFVVSTQLLNGSLAEGIIIRSENLTENTKTIIIVHLNES		
		301*	*	*350
SF162	(285)	VEINCTRPNNNTRKSVRIGPGQAFYATNDIIGNIRQAHCNISTDRWNKTL		
TV1.8_2	(299)	VEINCTRPNNNTRKSVRIGPGQAFYATNDIIGNIRQAHCNISTDRWNKTL		
TV1.8_5	(299)	VEINCTRPNNNTRKSVRIGPGQAFYATNDIIGNIRQAHCNISTDRWNKTL		
TV2.12-5/1	(285)	VEINCTRPNNNTRKSVRIGPGQAFYATNDIIGNIRQAHCNISTDRWNKTL		
Consensus	(301)	VEINCTRPNNNTRKSVRIGPGQAFYATNDIIGNIRQAHCNISTDRWNKTL		

FIGURE 105A

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		351	*		*	400	*
SF162	(335)	KQIVTKLQAQFGNKT-IVFKQSSGGPPTVMSTFNCGGEFFPYCHNTQLF					
TV1.8_2	(349)	QQVMKKLGEHFPNKT-IQFKPHAGGGLSTMTSTFNCGGEFFPYCHNTENLFT					
TV1.8_5	(349)	QQVMKKLGEHFPNKT-IKFEPHAGGGLSTMTSTFNCGGEFFPYCHNTENLFT					
TV2.12-5/1	(335)	QRVSQKLQELFPNSTGIKFAPHGGGLSTTSTFNCGGEFFPYCHNTTDLFT					
Consensus	(351)	QQVMKKLQEHFPNKT IKFKPHAGGGLSTMTSTFNCRGEFFPYCHNTENLFT					
		401	*	*		450	
SF162	(384)	STWNN-----TIGPN-NTNGTITLPORINQIINRGEVKAMYAPPIR					
TV1.8_2	(398)	STYHS---NNGTYKYNGNSSSPITLQCKIKQIVRMQGVQATYAPPIAG					
TV1.8_5	(398)	STYYP---KNGTYKYNGNSSLPITLQCKIKQIVRMQGVQAMAPPIAG					
TV2.12-5/1	(385)	STYSNGTCTNGTCMSN--NTERITLQCKIKQIINRMGEGRAMYAPPIAG					
Consensus	(401)	STYHN NGTYKYNGNSS PITLQCKIKQIIRMQGVQAMYPPIAG					
		451	*	*	*	500	
SF162	(427)	QIRCSNITGILLTRDGGKEISNT--TETFRPGGGDMRDNRSELYKYKV					
TV1.8_2	(445)	NITCRNITGILLTRDGGFNTTNN--TETFRPGGGDMRDNRSELYKYKV					
TV1.8_5	(445)	NITCRNITGILLTRDGGFNTTNDTE--TETFRPGGGDMRDNRSELYKYKV					
TV2.12-5/1	(433)	NITCRNITGILLTRDGGDNNTET---TETFRPGGGDMRDNRSELYKYKV					
Consensus	(451)	NITCRSNITGILLTRDGGFNTTNT TETFRPGGGDMRDNRSELYKYKV					
		501				550	
SF162	(475)	EKEPLGVAFTKAKRRVVQEKRAVIGAVFLGFLGAAGSTMGAASITLT					
TV1.8_2	(493)	EKEPLGIAPTKAKRRVVQEKRAVIGAVFLGFLGAAGSTMGAASITLT					
TV1.8_5	(495)	EKEPLGIAPTKAKRRVVQEKRAVIGAVFLGFLGAAGSTMGAASITLT					
TV2.12-5/1	(480)	EKEPLGVAFTKAKRRVVEEKRAVIGAVFLGFLGAAGSTMGAASITLT					
Consensus	(501)	VEIKPLGIAPTKAKRRVVQREKRAVIGAVFLGFLGAAGSTMGAASITLT					
		551				600	
SF162	(525)	VQARQLLSGIVQQSNLLRAIEAQQHMLQLTVWGIKQLQARVLAIERYLK					
TV1.8_2	(543)	VQARQLLSGIVQQSNLLRAIEAQQMQLTVWGIKQLQARVLAIERYLK					
TV1.8_5	(545)	VQARQLLSGIVQQSNLLRAIEAQQMQLTVWGIKQLQARVLAIERYLK					
TV2.12-5/1	(530)	VQARQLLSGIVQQSNLLRAIEAQQHMLQLTVWGIKQLQARVLAIEEYLQ					
Consensus	(551)	VQARQLLSGIVQQSNLLKAIEAQQHMLQLTVWGIKQLQARVLAIERYLK					
		601		*	*	650	*
SF162	(575)	DQQLLGIWCGSKLICCTTAVPWNSSWSNKSEADIWDNMTWMQWDREISNY					
TV1.8_2	(593)	DQQLLGIWCGSKLICCTTAVPWNSSWSNKSEADIWDNMTWMQWDREISNY					
TV1.8_5	(595)	DQQLLGIWCGSKLICCTTAVPWNSSWSNKSEADIWDNMTWMQWDREISNY					
TV2.12-5/1	(580)	DQQLLGIWCGSKLICCTNVLWNSSWSNKSEADIWDNMTWMQWDREISNY					
Consensus	(601)	DQQLLGIWCGSKLICCTTAVPWNSSWSNKSEADIWDNMTWMQWDREISNY					
		651				700	
SF162	(625)	NLYTYRLLEDSONQQEKNEKDLELDKNNLWNWFDISNLWYIKIFIMI					
TV1.8_2	(643)	GLYNYRLLEDSONQQEKNEKDLELDKNNLWNWFDISNPYIKIFIMI					
TV1.8_5	(645)	ETIYRLLEDSONQQEKNEKDLELDKNNLWNWFDISNLWYIKIFIMI					
TV2.12-5/1	(630)	NTIYRLLEDSONQQEKNEKDLELDKNNLWNWFDISNLWYIKIFIMI					
Consensus	(651)	TNTIYRLLEDSONQQEKNEKDLELDKNNLWNWFDISNLWYIKIFIMI					
		701				750	
SF162	(675)	VGGILGLRIIFAVLSIVNVRVQGYSPLSFQTLTPSPRGPDRLGGIEEEGG					
TV1.8_2	(693)	VGGILGLRIIFAVLSIVNVRVQGYSPLSFQTLTPSPGLDLGLGIEEEGG					
TV1.8_5	(695)	VGGILGLRIIFAVLSIVNVRVQGYSPLSFQTLTPSPGLDLGLGIEEEGG					
TV2.12-5/1	(680)	VGGILGLRIIFAVLSIANVRVQGYSPLSLQTLINPRGPDRLGIEEEGG					
Consensus	(701)	VGGILGLRIIFAVLSIVNVRVQGYSPLSFQTLTPSPRGPDRLGGIEEEGG					

FIGURE 105B

		751		800
SF162	(725)	ERDRDSSPIHGLIAINDDLSICLFSYHRLRDLIAAIVELGR-		
TV1.8_2	(743)	EQDRDSIRLVSGFLSANDLLENCLSYHRLRDFILIAVAVELLGHS		
TV1.8_5	(745)	EQDRDSIRLVSGFLSANDLLENCLSYHRLRDFILIAVAVELLGHS		
TV2.12-5/1	(730)	EQDSSRSIRLVSGFLTAWDDLNSICLFCYHRLRDFILIVVAVELLGHS		
Consensus	(751)	EQDRDSIRLVSGFLSLAWDDLRLCLFSYHRLRDFILIAVAVELLGHS		
		801		850
SF162	(774)	-----EALKYWNLLQYNIQELKNVSLFDALIAVAEGTDRIE		
TV1.8_2	(793)	SLRGLQGWELKYLGLSVQYWGLESKSAISLLDTIAIAVAEGTDRIE		
TV1.8_5	(795)	SLRGLQGWELKYLGLSVQYWGLESKSAISPLDTIAIAVAEGTDRIE		
TV2.12-5/1	(780)	SLRGLQGWGTLYLGLSVQYWGLESKSAINLLDTIAIAVAEGTDRIE		
Consensus	(801)	SLRGLQRGWEILKYLGLSVQYWGLESKSAISLLDTIAIAVAEGTDRIE		
		851		876
SF162	(818)	VAQRIGRAFLHIFRRIRQGFRAALL-		
TV1.8_2	(843)	LVQRICRAILNIPRRIRQGFRAALL-		
TV1.8_5	(845)	LVQRICRAILNIPRRIRQGFRAALL-		
TV2.12-5/1	(830)	FIGNLCRGIRNVRRIRQGFRAALLQ-		
Consensus	(851)	LVQRICRAILNIPRRIRQGFRAALL		

FIGURE 105C